```
  1 GTTATTTCAG GCCATGGTGT TGCGCCGAAT TAATTCCCGA TCCAGACATG ATAAGATACA TTGATGAGTT TGGACAAACC ACAACTAGAA TGCAGTGAAA
    CAATAAAGTC CGGTACCACA ACGCGGCTTA ATTAAGGGCT AGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTTGG TGTTGATCTT ACGTCACTTT

101 AAAATGCTTT ATTTGTGAAA TTTGTGATGC TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAAACAA GTTGGGCCAT GGCGGCCAAG CTTCTGCAGG
    TTTTACGAAA TAAACACTTT AAACACTACG ATAACGAAAT AAACATTGGT AATATTCGAC GTTATTTGTT CAACCCGGTA CCGCCGGTTC GAAGACGTCC

201 TCGACTCTAG AGGATCCCCG GGGAATTCCG GCATGACTCG ATCGCCGCCC CTCAGAGAGC TGCCCCCGAG TTACACACCC CCAGCTCGAA CCGCAGCACC
    AGCTGAGATC TCCTAGGGGC CCCTTAAGGC CGTACTGAGC TAGCGGCGGG GAGTCTCTCG ACGGGGGCTC AATGTGTGGG GGTCGAGCTT GGCGTCGTGG
  1                                   M  T  R  S  P  P  L  R  E  L  P  P  S  Y  T  P  P  A  R  T  A  A  P

301 CCAGATCCTA GCTGGGAGCC TGAAGGCTCC ACTCTGGCTT CGTGCTTACT TCCAGGGCCT GCTCTTCTCT CTGGGATGCG GGATCCAGAG ACATTGTGGC
    GGTCTAGGAT CGACCCTCGG ACTTCCGAGG TGAGACCGAA GCACGAATGA AGGTCCCGGA CGAGAAGAGA GACCCTACGC CCTAGGTCTC TGTAACACCG
 24 Q  I  L  A  G  S  L  K  A  P  L  W  L  R  A  Y  F  Q  G  L  L  F  S  L  G  C  G  I  Q  R  H  C  G

401 AAAGTGCTCT TTCTGGGACT GTTGGCCTTT GGGGCCCTGG CATTAGGTCT CCGCATGGCC ATTATTGAGA CAAACTTGGA ACAGCTCTGG GTAGAAGTGG
    TTTCACGAGA AAGACCCTGA CAACCGGAAA CCCCGGGACC GTAATCCAGA GGCGTACCGG TAATAACTCT GTTTGAACCT TGTCGAGACC CATCTTCACC
 57 K  V  L  F  L  G  L  L  A  F  G  A  L  A  L  G  L  R  M  A  I  I  E  T  N  L  E  Q  L  W  V  E  V  G

501 GCAGCCGGGT GAGCCAGGAG CTGCATTACA CCAAGGAGAA GCTGGGGGAG GAGGCTGCAT ACACCTCTCA GATGCTGATA CAGACCGCAC GCCAGGAGGG
    CGTCGGCCCA CTCGGTCCTC GACGTAATGT GGTTCCTCTT CGACCCCCTC CTCCGACGTA TGTGGAGAGT CTACGACTAT GTCTGGCGTG CGGTCCTCCC
 91   S  R  V  S  Q  E  L  H  Y  T  K  E  K  L  G  E  E  A  A  Y  T  S  Q  M  L  I  Q  T  A  R  Q  E  G

601 AGAGAACATC CTCACACCCG AAGCACTTGG CCTCCACCTC CAGGCAGCCC TCACTGCCAG TAAAGTCCAA GTATCACTCT ATGGGAAGTC CTGGGATTTG
    TCTCTTGTAG GAGTGTGGGC TTCGTGAACC GGAGGTGGAG GTCCGTCGGG AGTGACGGTC ATTTCAGGTT CATAGTGAGA TACCCTTCAG GACCCTAAAC
124 E  N  I  L  T  P  E  A  L  G  L  H  L  Q  A  A  L  T  A  S  K  V  Q  V  S  L  Y  G  K  S  W  D  L

701 AACAAAATCT GCTACAAGTC AGGAGTTCCC CTTATTGAAA ATGGAATGAT TGAGTGGATG ATTGAGAAGC TGTTTCCGTG CGTGATCCTC ACCCCCCTCG
    TTGTTTTAGA CGATGTTCAG TCCTCAAGGG GAATAACTTT TACCTTACTA ACTCACCTAC TAACTCTTCG ACAAAGGCAC GCACTAGGAG TGGGGGGAGC
157 N  K  I  C  Y  K  S  G  V  P  L  I  E  N  G  M  I  E  W  M  I  E  K  L  F  P  C  V  I  L  T  P  L  D
```

FIG._1A

```
801 ACTGCTTCTG GGAGGGAGCC AAACTCCAAG GGGGCTCCGC CTACCTGCCC GGCCGCCCGG ATATCCAGTG GACCAACCTG GATCCAGAGC AGCTGCTGGA
    TGACGAAGAC CCTCCCTCGG TTTGAGGTTC CCCCGAGGCG GATGGACGGG CCGGCGGGCC TATAGGTCAC CTGGTTGGAC CTAGGTCTCG TCGACGACCT
191   C  F  W  E  G  A  K  L  Q  G  G  S  A  Y  L  P  G  R  P  D  I  Q  W  T  N  L  D  P  E  Q  L  L  E

901 GGAGCTGGGT CCCTTTGCCT CCCTTGAGGG CTTCCGGGAG CTGCTAGACA AGGCACAGGT GGGCCAGGCC TACGTGGGGC GGCCCTGTCT GCACCCTGAT
    CCTCGACCCA GGGAAACGGA GGGAACTCCC GAAGGCCCTC GACGATCTGT TCCGTGTCCA CCCGGTCCGG ATGCACCCCG CCGGGACAGA CGTGGGACTA
224 E  L  G  P  F  A  S  L  E  G  F  R  E  L  L  D  K  A  Q  V  G  Q  A  Y  V  G  R  P  C  L  H  P  D

1001 GACCTCCACT GCCCACCTAG TGCCCCCAAC CATCACAGCA GGCAGGCTCC CAATGTGGCT CACGAGCTGA GTGGGGGCTG CCATGGCTTC TCCCACAAAT
     CTGGAGGTGA CGGGTGGATC ACGGGGGTTG GTAGTGTCGT CCGTCCGAGG GTTACACCGA GTGCTCGACT CACCCCCGAC GGTACCGAAG AGGGTGTTTA
257 D  L  H  C  P  P  S  A  P  N  H  H  S  R  Q  A  P  N  V  A  H  E  L  S  G  G  C  H  G  F  S  H  K  F

1101 TCATGCACTG GCAGGAGGAA TTGCTGCTGG GAGGCATGGC CAGAGACCCC CAAGGAGAGC TGCTGAGGGC AGAGGCCCTG CAGAGCACCT TCTTGCTGAT
     AGTACGTGAC CGTCCTCCTT AACGACGACC CTCCGTACCG GTCTCTGGGG GTTCCTCTCG ACGACTCCCG TCTCCGGGAC GTCTCGTGGA AGAACGACTA
291   M  H  W  Q  E  E  L  L  L  G  G  M  A  R  D  P  Q  G  E  L  L  R  A  E  A  L  Q  S  T  F  L  L  M

1201 GAGTCCCCGC CAGCTGTACG AGCATTTCCG GGGTGACTAT CAGACACATG ACATTGGCTG GAGTGAGGAG CAGGCCAGCA CAGTGCTACA AGCCTGGCAG
     CTCAGGGGCG GTCGACATGC TCGTAAAGGC CCCACTGATA GTCTGTGTAC TGTAACCGAC CTCACTCCTC GTCCGGTCGT GTCACGATGT TCGGACCGTC
324 S  P  R  Q  L  Y  E  H  F  R  G  D  Y  Q  T  H  D  I  G  W  S  E  E  Q  A  S  T  V  L  Q  A  W  Q

1301 CGGCGCTTTG TGCAGCTGGC CCAGGAGGCC CTGCCTGAGA ACGCTTCCCA GCAGATCCAT GCCTTCTCCT CCACCACCCT GGATGACATC CTGCATGCGT
     GCCGCGAAAC ACGTCGACCG GGTCCTCCGG GACGGACTCT TGCGAAGGGT CGTCTAGGTA CGGAAGAGGA GGTGGTGGGA CCTACTGTAG GACGTACGCA
357 R  R  F  V  Q  L  A  Q  E  A  L  P  E  N  A  S  Q  Q  I  H  A  F  S  S  T  T  L  D  D  I  L  H  A  F

1401 TCTCTGAAGT CAGTGCTGCC CGTGTGGTGG GAGGCTATCT GCTCATGCTG GCCTATGCCT GTGTGACCAT GCTGCGGTGG GACTGCGCCC AGTCCCAGGG
     AGAGACTTCA GTCACGACGG GCACACCACC CTCCGATAGA CGAGTACGAC CGGATACGGA CACACTGGTA CGACGCCACC CTGACGCGGG TCAGGGTCCC
391   S  E  V  S  A  A  R  V  V  G  G  Y  L  L  M  L  A  Y  A  C  V  T  M  L  R  W  D  C  A  Q  S  Q  G

1501 TTCCGTGGGC CTTGCCGGGG TACTGCTGGT GGCCCTGGCG GTGGCCTCAG GCCTTGGGCT CTGTGCCCTG CTCGGCATCA CCTTCAATGC TGCCACTACC
     AAGGCACCCG GAACGGCCCC ATGACGACCA CCGGGACCGC CACCGGAGTC CGGAACCCGA GACACGGGAC GAGCCGTAGT GGAAGTTACG ACGGTGATGG
424 S  V  G  L  A  G  V  L  L  V  A  L  A  V  A  S  G  L  G  L  C  A  L  L  G  I  T  F  N  A  A  T  T
```

FIG._1B

```
1601 CAGGTGCTGC CTTTCTTGGC TCTGGGAATC GGCGTGGATG ACGTATTCCT GCTGGCGCAT GCCTTCACAG AGGCTCTGCC TGGCACCCCT CTCCAGGAGC
     GTCCACGACG GAAAGAACCG AGACCCTTAG CCGCACCTAC TGCATAAGGA CGACCGCGTA CGGAAGTGTC TCCGAGACGG ACCGTGGGGA GAGGTCCTCG
 457 Q  V  L  P  F  L  A  L  G  I  G  V  D  D  V  F  L  L  A  H  A  F  T  E  A  L  P  G  T  P  L  Q  E  R

1701 GCATGGGCGA GTGTCTGCAG CGCACGGGCA CCAGTGTCGT ACTCACATCC ATCAACAACA TGGCCGCCTT CCTCATGGCT GCCCTCGTTC CCATCCCTGC
     CGTACCCGCT CACAGACGTC GCGTGCCCGT GGTCACAGCA TGAGTGTAGG TAGTTGTTGT ACCGGCGGAA GGAGTACCGA CGGGAGCAAG GGTAGGGACG
  491  M  G  E  C  L  Q  R  T  G  T  S  V  V  L  T  S  I  N  N  M  A  A  F  L  M  A  A  L  V  P  I  P  A

1801 GCTGCGAGCC TTCTCCCTAC AGGCGGCCAT AGTGGTTGGC TGCACCTTTG TAGCCGTGAT GCTTGTCTTC CCAGCCATCC TCAGCCTGGA CCTACGGCGG
     CGACGCTCGG AAGAGGGATG TCCGCCGGTA TCACCAACCG ACGTGGAAAC ATCGGCACTA CGAACAGAAG GGTCGGTAGG AGTCGGACCT GGATGCCGCC
 524 L  R  A  F  S  L  Q  A  A  I  V  V  G  C  T  F  V  A  V  M  L  V  F  P  A  I  L  S  L  D  L  R  R

1901 CGCCACTGCC AGCGCCTTGA TGTGCTCTGC TGCTTCTCCA GTCCCTGCTC TGCTCAGGTG ATTCAGATCC TGCCCCAGGA GCTGGGGGAC GGGACAGTAC
     GCGGTGACGG TCGCGGAACT ACACGAGACG ACGAAGAGGT CAGGGACGAG ACGAGTCCAC TAAGTCTAGG ACGGGGTCCT CGACCCCCTG CCCTGTCATG
 557 R  H  C  Q  R  L  D  V  L  C  C  F  S  S  P  C  S  A  Q  V  I  Q  I  L  P  Q  E  L  G  D  G  T  V  P

2001 CAGTGGGCAT TGCCCACCTC ACTGCCACAG TTCAAGCCTT TACCCACTGT GAAGCCAGCA GCCAGCATGT GGTCACCATC CTGCCTCCCC AAGCCCACCT
     GTCACCCGTA ACGGGTGGAG TGACGGTGTC AAGTTCGGAA ATGGGTGACA CTTCGGTCGT CGGTCGTACA CCAGTGGTAG GACGGAGGGG TTCGGGTGGA
  591  V  G  I  A  H  L  T  A  T  V  Q  A  F  T  H  C  E  A  S  S  Q  H  V  V  T  I  L  P  P  Q  A  H  L

2101 GGTGCCCCCA CCTTCTGACC CACTGGGCTC TGAGCTCTTC AGCCCTGGAG GGTCCACACG GGACCTTCTA GGCCAGGAGG AGGAGACAAG GCAGAAGGCA
     CCACGGGGGT GGAAGACTGG GTGACCCGAG ACTCGAGAAG TCGGGACCTC CCAGGTGTGC CCTGGAAGAT CCGGTCCTCC TCCTCTGTTC CGTCTTCCGT
  624  V  P  P  P  S  D  P  L  G  S  E  L  F  S  P  G  G  S  T  R  D  L  L  G  Q  E  E  E  T  R  Q  K  A

2201 GCCTGCAAGT CCCTGCCCTG TGCCCGCTGG AATCTTGCCC ATTTCGCCCG CTATCAGTTT GCCCCGTTGC TGCTCCAGTC ACATGCCAAG GCCATCGTGC
     CGGACGTTCA GGGACGGGAC ACGGGCGACC TTAGAACGGG TAAAGCGGGC GATAGTCAAA CGGGGCAACG ACGAGGTCAG TGTACGGTTC CGGTAGCACG
 657 A  C  K  S  L  P  C  A  R  W  N  L  A  H  F  A  R  Y  Q  F  A  P  L  L  L  Q  S  H  A  K  A  I  V  L

2301 TGGTGCTCTT TGGTGCTCTT CTGGGCCTGA GCCTCTACGG AGCCACCTTG GTGCAAGACG GCCTGGCCCT GACGGATGTG GTGCCTCGGG GCACCAAGGA
     ACCACGAGAA ACCACGAGAA GACCCGGACT CGGAGATGCC TCGGTGGAAC CACGTTCTGC CGGACCGGGA CTGCCTACAC CACGGAGCCC CGTGGTTCCT
  691  V  L  F  G  A  L  L  G  L  S  L  Y  G  A  T  L  V  Q  D  G  L  A  L  T  D  V  V  P  R  G  T  K  E
```

FIG._1C

```
2401 GCATGCCTTC CTGAGCGCCC AGCTCAGGTA CTTCTCCCTG TACGAGGTGG CCCTGGTGAC CCAGGGTGGC TTTGACTACG CCCATTCCCA ACGCGCCCTC
     CGTACGGAAG GACTCGCGGG TCGAGTCCAT GAAGAGGGAC ATGCTCCACC GGGACCACTG GGTCCCACCG AAACTGATGC GGGTAAGGGT TGCGCGGGAG
 724 H  A  F  L  S  A  Q  L  R  Y  F  S  L  Y  E  V  A  L  V  T  Q  G  G  F  D  Y  A  H  S  Q  R  A  L

2501 TTTGATCTGC ACCAGCGCTT CAGTTCCCTC AAGGCGGTGC TGCCCCCACC GGCCACCCAG GCACCCCGCA CCTGGCTGCA CTATTACCGC AACTGGCTAC
     AAACTAGACG TGGTCGCGAA GTCAAGGGAG TTCCGCCACG ACGGGGGTGG CCGGTGGGTC CGTGGGGCGT GGACCGACGT GATAATGGCG TTGACCGATG
 757 F  D  L  H  Q  R  F  S  S  L  K  A  V  L  P  P  P  A  T  Q  A  P  R  T  W  L  H  Y  Y  R  N  W  L  Q

2601 AGGGAATCCA GGCTGCCTTT GACCAGGACT GGGCTTCTGG GCGCATCACC CGCCACTCGT ACCGCAATGG CTCTGAGGAT GGGGCCCTGG CCTACAAGCT
     TCCCTTAGGT CCGACGGAAA CTGGTCCTGA CCCGAAGACC CGCGTAGTGG GCGGTGAGCA TGGCGTTACC GAGACTCCTA CCCCGGGACC GGATGTTCGA
 791   G  I  Q  A  A  F  D  Q  D  W  A  S  G  R  I  T  R  H  S  Y  R  N  G  S  E  D  G  A  L  A  Y  K  L

2701 GCTCATCCAG ACTGGAGACG CCCAGGAGCC TCTGGATTTC AGCCAGCTGA CCACAAGGAA GCTGGTGGAC AGAGAGGGAC TGATTCCACC CGAGCTCTTC
     CGAGTAGGTC TGACCTCTGC GGGTCCTCGG AGACCTAAAG TCGGTCGACT GGTGTTCCTT CGACCACCTG TCTCTCCCTG ACTAAGGTGG GCTCGAGAAG
 824 L  I  Q  T  G  D  A  Q  E  P  L  D  F  S  Q  L  T  T  R  K  L  V  D  R  E  G  L  I  P  P  E  L  F

2801 TACATGGGGC TGACCGTGTG GGTGAGCAGT GACCCCCTGG GTCTGGCAGC CTCACAGGCC AACTTCTACC CCCCACCTCC TGAATGGCTG CACGACAAAT
     ATGTACCCCG ACTGGCACAC CCACTCGTCA CTGGGGGACC CAGACCGTCG GAGTGTCCGG TTGAAGATGG GGGGTGGAGG ACTTACCGAC GTGCTGTTTA
 857 Y  M  G  L  T  V  W  V  S  S  D  P  L  G  L  A  A  S  Q  A  N  F  Y  P  P  P  P  E  W  L  H  D  K  Y

2901 ACGACACCAC GGGGGAGAAC CTTCGCATCC CGCCAGCTCA GCCCTTGGAG TTTGCCCAGT TCCCCTTCCT GCTGCGTGGC CTCCAGAAGA CTGCAGACTT
     TGCTGTGGTG CCCCCTCTTG GAAGCGTAGG GCGGTCGAGT CGGGAACCTC AAACGGGTCA AGGGGAAGGA CGACGCACCG GAGGTCTTCT GACGTCTGAA
 891   D  T  T  G  E  N  L  R  I  P  P  A  Q  P  L  E  F  A  Q  F  P  F  L  L  R  G  L  Q  K  T  A  D  F

3001 TGTGGAGGCC ATCGAGGGGG CCCGGGCAGC ATGCGCAGAG GCCGGCCAGG CTGGGGTGCA CGCCTACCCC AGCGGCTCCC CCTTCCTCTT CTGGGAACAG
     ACACCTCCGG TAGCTCCCCC GGGCCCGTCG TACGCGTCTC CGGCCGGTCC GACCCCACGT GCGGATGGGG TCGCCGAGGG GGAAGGAGAA GACCCTTGTC
 924 V  E  A  I  E  G  A  R  A  A  C  A  E  A  G  Q  A  G  V  H  A  Y  P  S  G  S  P  F  L  F  W  E  Q

3101 TATCTGGGCC TGCGGCGCTG CTTCCTGCTG GCCGTCTGCA TCCTGCTGGT GTGCACTTTC CTCGTCTGTG CTCTGCTGCT CCTCAACCCC TGGACGGCTG
     ATAGACCCGG ACGCCGCGAC GAAGGACGAC CGGCAGACGT AGGACGACCA CACGTGAAAG GAGCAGACAC GAGACGACGA GGAGTTGGGG ACCTGCCGAC
 957 Y  L  G  L  R  R  C  F  L  L  A  V  C  I  L  L  V  C  T  F  L  V  C  A  L  L  L  L  N  P  W  T  A  G
```

FIG._1D

```
3201 GCCTCATAGT GCTGGTCCTG GCGATGATGA CAGTGGAACT CTTTGGTATC ATGGGTTTCC TGGGCATCAA GCTGAGTGCC ATCCCCGTGG TGATCCTTGT
     CGGAGTATCA CGACCAGGAC CGCTACTACT GTCACCTTGA GAAACCATAG TACCCAAAGG ACCCGTAGTT CGACTCACGG TAGGGGCACC ACTAGGAACA
 991   L  I  V  L  V  L  A  M  M  T  V  E  L  F  G  I  M  G  F  L  G  I  K  L  S  A  I  P  V  V  I  L  V

3301 GGCCTCTGTA GGCATTGGCG TTGAGTTCAC AGTCCACGTG GCTCTGGGCT TCCTGACCAC CCAGGGCAGC CGGAACCTGC GGGCCGCCCA TGCCCTTGAG
     CCGGAGACAT CCGTAACCGC AACTCAAGTG TCAGGTGCAC CGAGACCCGA AGGACTGGTG GGTCCCGTCG GCCTTGGACG CCCGGCGGGT ACGGGAACTC
1024  A  S  V  G  I  G  V  E  F  T  V  H  V  A  L  G  F  L  T  T  Q  G  S  R  N  L  R  A  A  H  A  L  E

3401 CACACATTTG CCCCCGTGAC CGATGGGGCC ATCTCCACAT TGCTGGGTCT GCTCATGCTT GCTGGTTCCC ACTTTGACTT CATTGTAAGG TACTTCTTTG
     GTGTGTAAAC GGGGGCACTG GCTACCCCGG TAGAGGTGTA ACGACCCAGA CGAGTACGAA CGACCAAGGG TGAAACTGAA GTAACATTCC ATGAAGAAAC
1057 H  T  F  A  P  V  T  D  G  A  I  S  T  L  L  G  L  L  M  L  A  G  S  H  F  D  F  I  V  R  Y  F  F  A

3501 CGGCGCTGAC AGTGCTCACG CTCCTGGGCC TCCTCCATGG ACTCGTGCTG CTGCCTGTGC TGCTGTCCAT CCTGGGCCCG CCGCCAGAGG TGATACAGAT
     GCCGCGACTG TCACGAGTGC GAGGACCCGG AGGAGGTACC TGAGCACGAC GACGGACACG ACGACAGGTA GGACCCGGGC GGCGGTCTCC ACTATGTCTA
1091  A  L  T  V  L  T  L  L  G  L  L  H  G  L  V  L  L  P  V  L  L  S  I  L  G  P  P  P  E  V  I  Q  M

3601 GTACAAGGAA AGCCCAGAGA TCCTGAGTCC ACCAGCTCCA CAGGGAGGCG GGCTTAGGTG GGGGGCATCC TCCTCCCTGC CCCAGAGCTT TGCCAGAGTG
     CATGTTCCTT TCGGGTCTCT AGGACTCAGG TGGTCGAGGT GTCCCTCCGC CCGAATCCAC CCCCCGTAGG AGGAGGGACG GGGTCTCGAA ACGGTCTCAC
1124  Y  K  E  S  P  E  I  L  S  P  P  A  P  Q  G  G  G  L  R  W  G  A  S  S  S  L  P  Q  S  F  A  R  V

3701 ACTACCTCCA TGACCGTGGC CATCCACCCA CCCCCCCTGC CTGGTGCCTA CATCCATCCA GCCCCTGATG AGCCCCCTTG GTCCCCTGCT GCCACTAGCT
     TGATGGAGGT ACTGGCACCG GTAGGTGGGT GGGGGGGACG GACCACGGAT GTAGGTAGGT CGGGGACTAC TCGGGGGAAC CAGGGGACGA CGGTGATCGA
1157 T  T  S  M  T  V  A  I  H  P  P  P  L  P  G  A  Y  I  H  P  A  P  D  E  P  P  W  S  P  A  A  T  S  S

3801 CTGGCAACCT CAGTTCCAGG GGACCAGGTC CAGCCACTGG GTGAAAGAGC AGCTGAAGCA CAGAGACCAT GTGTGGGGCG TGTGGGGTCA CTGGGAAGCA
     GACCGTTGGA GTCAAGGTCC CCTGGTCCAG GTCGGTGACC CACTTTCTCG TCGACTTCGT GTCTCTGGTA CACACCCCGC ACACCCCAGT GACCCTTCGT
1191  G  N  L  S  S  R  G  P  G  P  A  T  G  O

3901 CTGGGTCTGG TGTTAGACGC AGGACGGACC CCTGGAGGGC CCTGCTGCTG CTGCATCCCC TCTCCCGACC CAGCTGTCAT GGGCCTCCCT GATATCGAAT
     GACCCAGACC ACAATCTGCG TCCTGCCTGG GGACCTCCCG GGACGACGAC GACGTAGGGG AGAGGGCTGG GTCGACAGTA CCCGGAGGGA CTATAGCTTA

4001 TCAATCGATA GAACCGAGGT GCAGTTGGAC
     AGTTAGCTAT CTTGGCTCCA CGTCAACCTG
```

FIG._1E

```
                30         40         50         60         70
905531      GCTGGGGTGCACGCCTACCNCAGCGGNTCCCCCTTCCTCTTCTGGGAACA
              ::: ::   :   ******* ***** ******************** **
hpatched    CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA
          3010       3020       3030       3040       3050

                80         90        100        110        120
905531      GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
            ***  * ***** ** * ***  * ******  * ** ** *  ** ***
hpatched    GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTCATCAGCGTGGTGTTGG
          3060       3070       3080       3090       3100

                130        140        150        160        170
905531      TGTGCACTTTCCTCGTCTGTGCTCTGCTGCTCCTNAACCCCTGGACGGCT
              ***** ******** ** *** *  * ** ****************
hpatched    CCTGCACATTCCTCGTGTGCGCTGTCTTCCTTCTGAACCCCTGGACGGCC
          3110       3120       3130       3140       3150

                180        190        200        210        220
905531      GGCCTNATAGTGCTGGTCCTGGCGATGATGACAGTGGAACTCTTTGGTAT
            **  **** *** ********** ******* ** ** ** ** ** **
hpatched    GGGATCATTGTGATGGTCCTGGCGCTGATGACGGTCGAGCTGTTCGGCAT
          3160       3170       3180       3190       3200

                230        240        250
905531      CATGGGTTTNCTGGGCATCAAGCTGAGT
             *****  ** * ** ******** ***
hpatched    GATGGGCCTCATCGGAATCAAGCTCAGT
          3210       3220       3230
```

```
                80         90        100        110        120
905531      TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
             :::   :::      * ** *  ** *****   ****   * ** ****
hpatched    GCTGCTGCTGTTCATCAGCGTGGTGTTGGCC---TGCACATTCCTCGTGT
                  3090       3100       3110       3120

              130        140        150
905531      GCACTTTCCTCGTCTGTGCTCTGCTGCT
            ** ** ** ** *       :    :
hpatched    GCGCTGTCTTCCTTCTGAACCCCTGGAC
          3130       3140       3150
```

FIG._2A

```
            30        40        50        60        70
1326258     GCTGGGGTGCACGCCTACCCCAGCGGCTCCCCCTTCCTCTTCTGGGAACA
               ::: ::  :   ******* ***** ****************** **
hpatched    CTGGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTCTGGGAGCA
          3010      3020      3030      3040      3050

            80        90       100       110       120
1326258     GTATCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGG
            ***  * ***** ** * ***  * ******  * ** ** *  ** ***
hpatched    GTACATCGGCCTCCGCCACTGGCTGCTGCTGTTCATCAGCGTGGTGTTGG
          3060      3070      3080      3090      3100

           130       140       150
1326258     TGTGCACTTTCCTCNTCTGTGCTCT
              ***** ******** ** *** *
hpatched    CCTGCACATTCCTCGTGTGCGCTGT
          3110      3120      3130
```

```
                  90       100       110       120       130
1326258     TCTGGGCCTGCGGCGCTGCTTCCTGCTGGCCGTCTGCATCCTGCTGGTGT
             :::   :::     * ** *  ** *****   ****   * ** ****
hpatched    GCTGCTGCTGTTCATCAGCGTGGTGTTGGCC---TGCACATTCCTCGTGT
                  3090      3100      3110          3120

               140       150
1326258     GCACTTTCCTCNTCTGTGCTCT
            ** ** ** ****       :
hpatched    GCGCTGTCTTCCTTCTGAACCC
          3130      3140
```

```
                  10        20        30        40        50
1326258       CCGGGCAGCATGCGCAGAGGCCGGCCAGGCTGGGGTGCACGCCTACCCCA
              ****** *****    ** ** * *** ******* *     :
hpatched.RC   CCGGGCGGCATG--GCGAAGCGGACCACGCTGGGGGGTGGCTCAGGGGAG
            710       720       730       740       750
```

FIG._2B

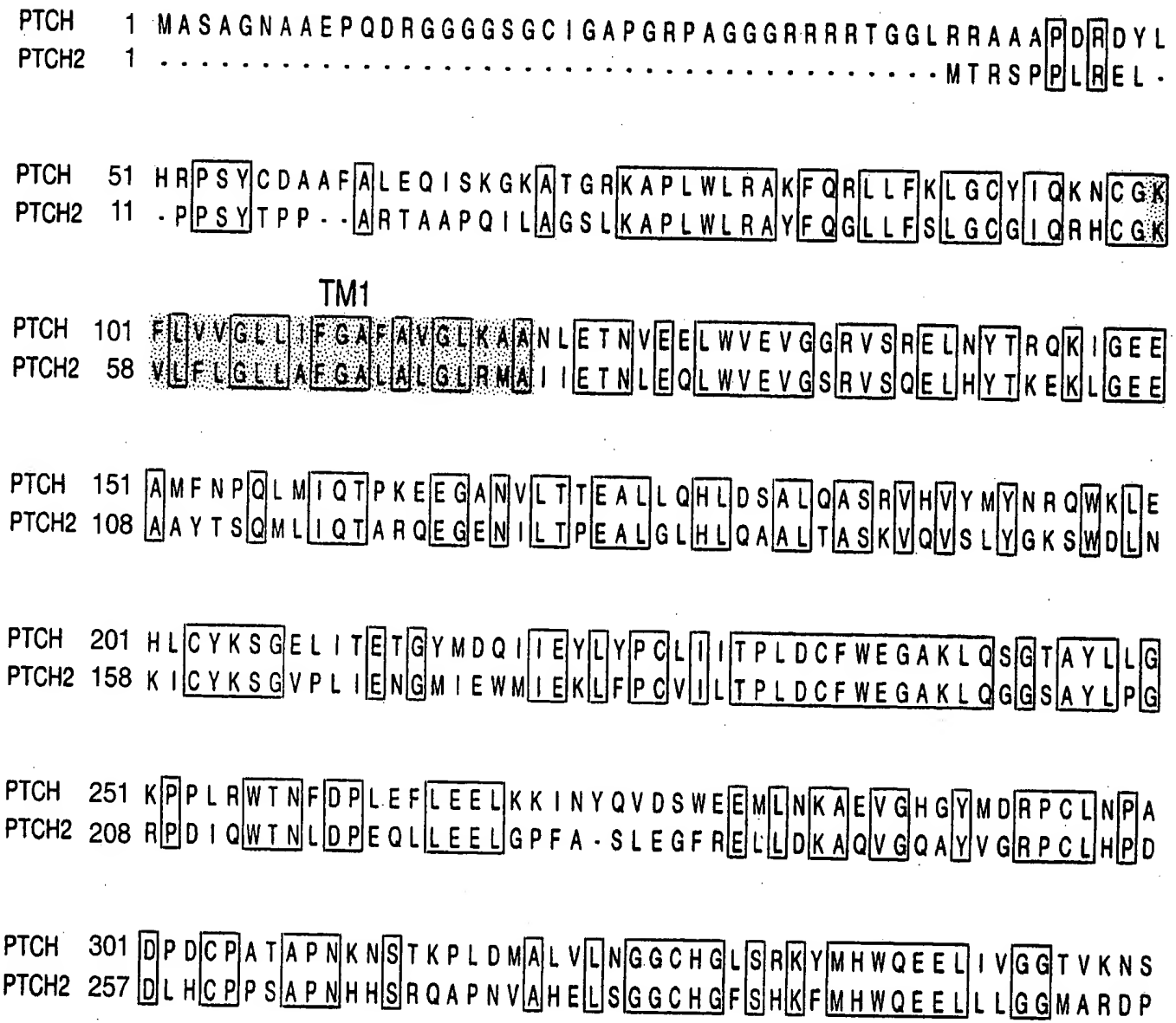
PTCH 1 MASAGNAAEPQDRGGGGSGCIGAPGRPAGGGRRRRTGGLRRAAAPDRDYL
PTCH2 1 ----------MTRSPPLRELR
PTCH 51 HRPSYCDAAFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGK
PTCH2 11 PPSYTPP--ARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCGIQRHCGK
TM1
PTCH 101 FLVVGLLIFGAFAVGLKAANLETNVEELWVEVGGRVSRELNYTRQKIGEE
PTCH2 58 VLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYTKEKLGEE
PTCH 151 AMFNPQLMIQTPKEEGANVLTTEALLQHLDSALQASRVHVYMYNRQWKLE
PTCH2 108 AAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLN
PTCH 201 HLCYKSGELITETGYMDQIIEYLYPCLIITPLDCFWEGAKLQSGTAYLLG
PTCH2 158 KICYKSGVPLIENGMIEWMIEKLFPCVILTPLDCFWEGAKLQGGSAYLPG
PTCH 251 KPPLRWTNFDPLEFLEELKKINYQVDSWEEMLNKAEVGHGYMDRPCLNPA
PTCH2 208 RPDIQWTNLDPEQLLEELGPFA-SLEGFRELLDKAQVGQAYVGRPCLHPD
PTCH 301 DPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTVKNS
PTCH2 257 DLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLGGMARDP

FIG._3A


PTCH 351 TGKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSH-INWNEDKAAAILEAW
PTCH2 307 QGELLRAEALQSTFLLMSPRQLYEHFRG-DYQTHDIGWSEEQASTVLQAW
TM2
PTCH 400 QRTYVEVVHQSVAQNSTQKVLSFTTTTLDDILKSFSDVSVIRVASGYLLM
PTCH2 356 QRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLM
TM3
PTCH 450 LAYACLTMLRWDCSKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAAT
PTCH2 406 LAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGITFNAAT
TM4
PTCH 500 TQVLPFLALGVGVDDVFLLAHAFSETGQNKRIPFEDRTGECLKRTGASVA
PTCH2 456 TQVLPFLALGIGVDDVFLLAHAFTEALPG--TPLQERMGECLQRTGTSVV
TM5
TM6
PTCH 550 LTSISNVTAFFMAALIPIPALRAFSLQAAVVVFNFAMVLLIFPAILSMD
PTCH2 504 LTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAILSLD
PTCH 600 LYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPPPPYSSHS
PTCH2 554 LRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGT----------VPVG
PTCH 650 FAHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDTLSC
PTCH2 593 IAH-----LTATVQAFTHCEASSQHVVTILPPQAHLVPPP----SDPLGS

FIG._3B


TM7
***
TM8
PTCH 700 QSPESTSSTRDLLSQFSDSSLH--CLEPPCTKWTLSSFAEKHYAPFLLKP
PTCH2 634 ELFSPGGSTRDLLGQEEETRQKAACKSLPCARWNLAHFARYQFAPLLLQS
PTCH 748 KAKVVVIFLFLGLLGVSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKY
PTCH2 684 HAKAIVLVLFGALLGLSLYGATLVQDGLALTDVVPRGTKEHAFLSAQLRY
PTCH 798 FSFYNMYIVTQKA-DYPNIQHLLYDLHRSFSNVKYVMLEENKQLPKMWLH
PTCH2 734 FSLYEVALVTQGGFDYAHSQRALFDLHQRFSSLKAVLPPPATQAPRTWLH
PTCH 847 YFRDWLQGLQDAFDSDWETGKIMPNNYKNGSDDGVLAYKLLVQTGSRDKP
PTCH2 784 YYRNWLQGIQAAFDQDWASGRITRHSYRNGSEDGALAYKLLIQTGDAQEP
PTCH 897 IDISQLTKQRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQANIRPHRP
PTCH2 834 LDFSQLTTRKLVDREGLIPPELFYMGLTVWVSSDPLGLAASQANFYPPPP
PTCH 947 EWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRT
PTCH2 884 EWLHDKYD-TTGENLRIPPAQPLEFAQFPFLLRGLQKTADFVEAIEGARA
PTCH 997 ICSNYTSLGLSSYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVF
PTCH2 933 ACAEAGQAGVHAYPSGSPFLFWEQYLGLRRCFLLAVCILLVCTFLVCALL

FIG._3C

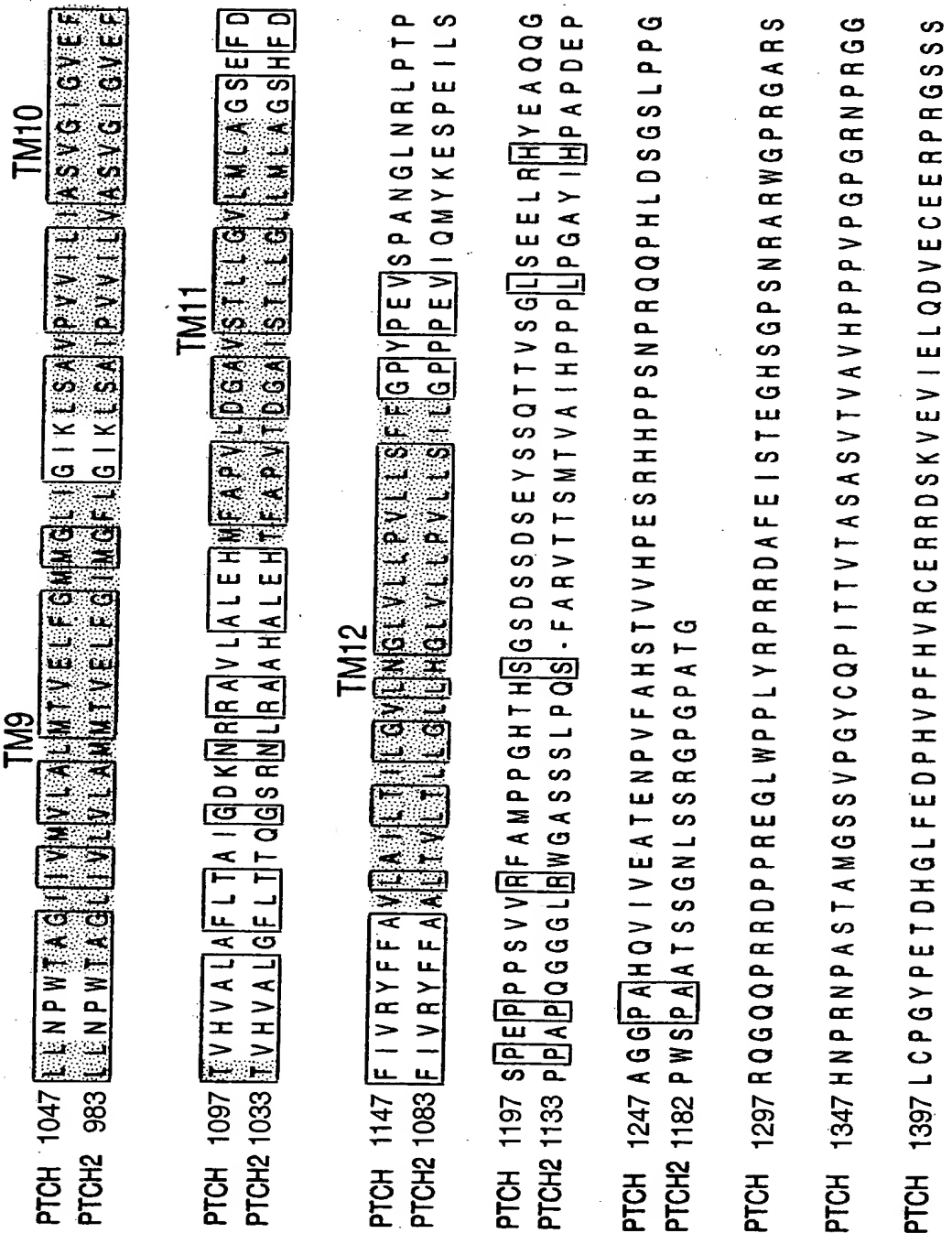
TM9
TM10
TM11
TM12
PTCH 1047 L L N P W T A G I I V M V L A L M T V E L F G M M G L I G I K L S A V P V V I L I A S V G I G V E F
PTCH2 983 L L N P W T A G L I V L V L A W M T V E L F G I M G F L G I K L S A I P V V I L V A S V G I G V E F
PTCH 1097 T V H V A L A F L T A I G D K N R R A V L A L E H M F A P V L D G A V S T L L G V L M L A G S E F D
PTCH2 1033 T V H V A L G F L T T Q G S R N L R A A H A L E H T F A P V T D G A I S T L L G L L M L A G S H F D
PTCH 1147 F I V R Y F F A V I A I L T I L G V I N S L V L L P V L I S F F G P Y P E V S P A N G L N R L P T P
PTCH2 1083 F I V R Y F F A L T V L T L L G L L H G L V L L P V L I S I L G P P E V I Q M Y K E S P E I L S
PTCH 1197 S P E P P P S V V R F A M P P G H T H S G S D S S D S E Y S S Q T T V S G L S E E L R H Y E A Q Q G
PTCH2 1133 P P A P Q G G G L R W G A S S S L P Q S - F A R V T T S M T V A I H P P P L P G A Y I H P A P D E P
PTCH 1247 A G G P A H Q V I V E A T E N P V F A H S T V V H P E S R H H P P S N P R Q Q P H L D S G S L P P G
PTCH2 1182 P W S P A A T S S G N L S S R G P G P A T G
PTCH 1297 R Q G Q Q P R R D P P R E G L W P P L Y R P R R D A F E I S T E G H S G P S N R A R W G P R G A R S
PTCH 1347 H N P R N P A S T A M G S S V P G Y C Q P I T T V T A S A S V T V A V H P P P V P G P G R N P R G G
PTCH 1397 L C P G Y P E T D H G L F E D P H V P F H V R C E R R D S K V E V I E L Q D V E C E E R P R G S S S
PTCH 1447 N

FIG._3D

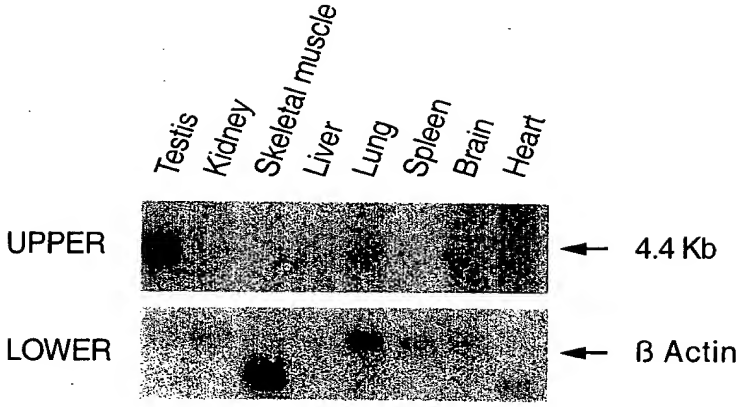
Testis
Kidney
Skeletal muscle
Liver
Lung
Spleen
Brain
Heart
UPPER
4.4 Kb
LOWER
ß Actin

FIG._4

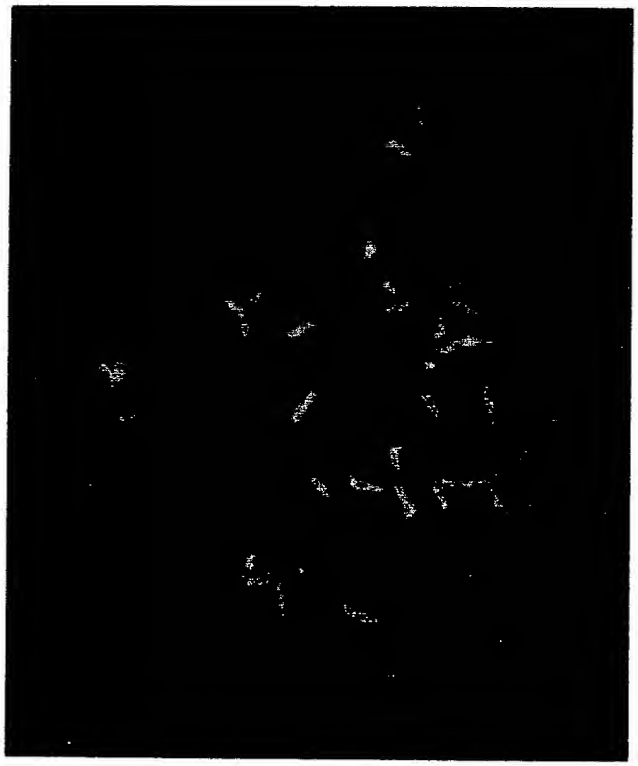

FIG._5

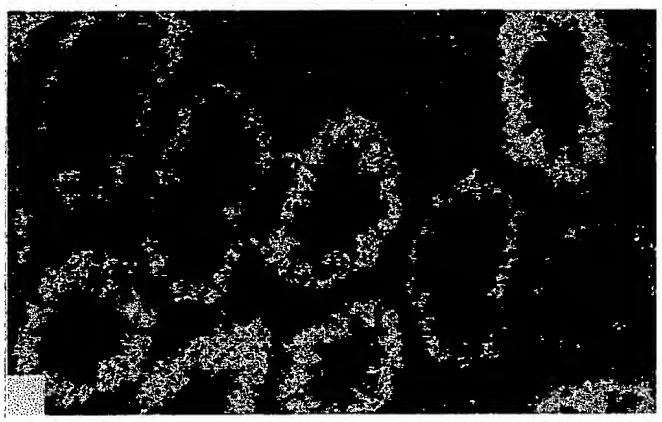

FIG._6C

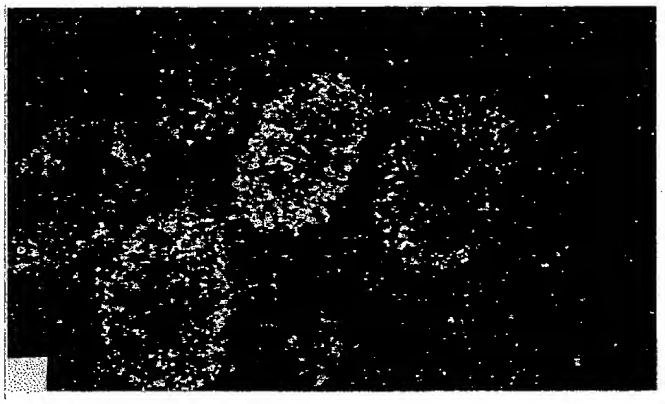

FIG._6B

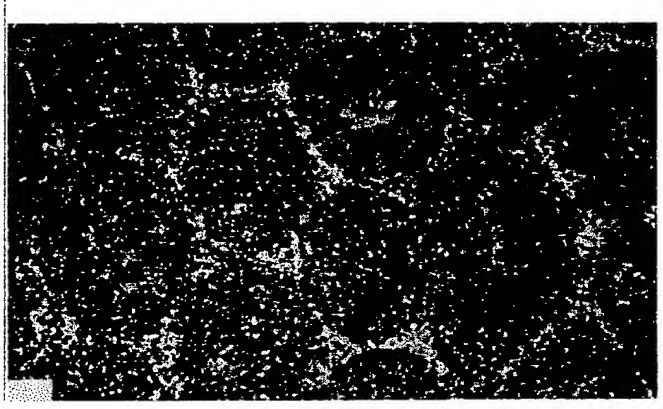

FIG._6A

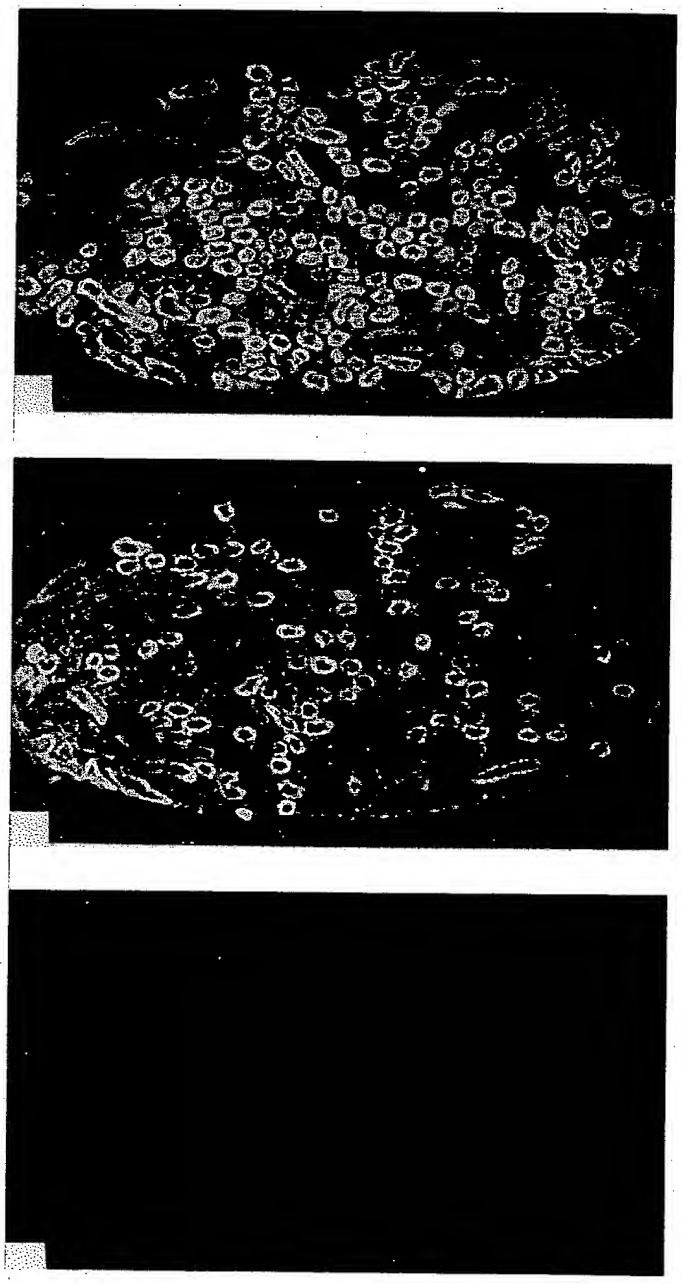

FIG._6F

FIG._6E

FIG._6D

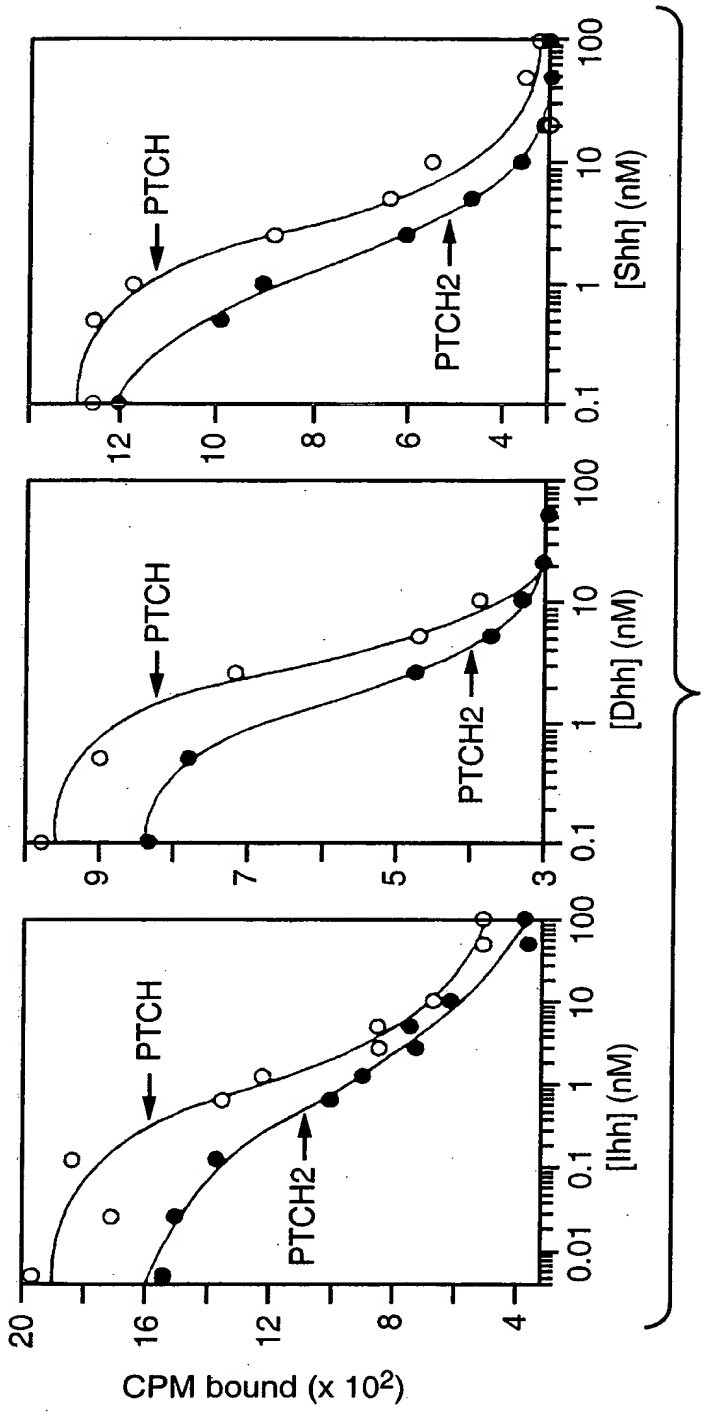

FIG._7A

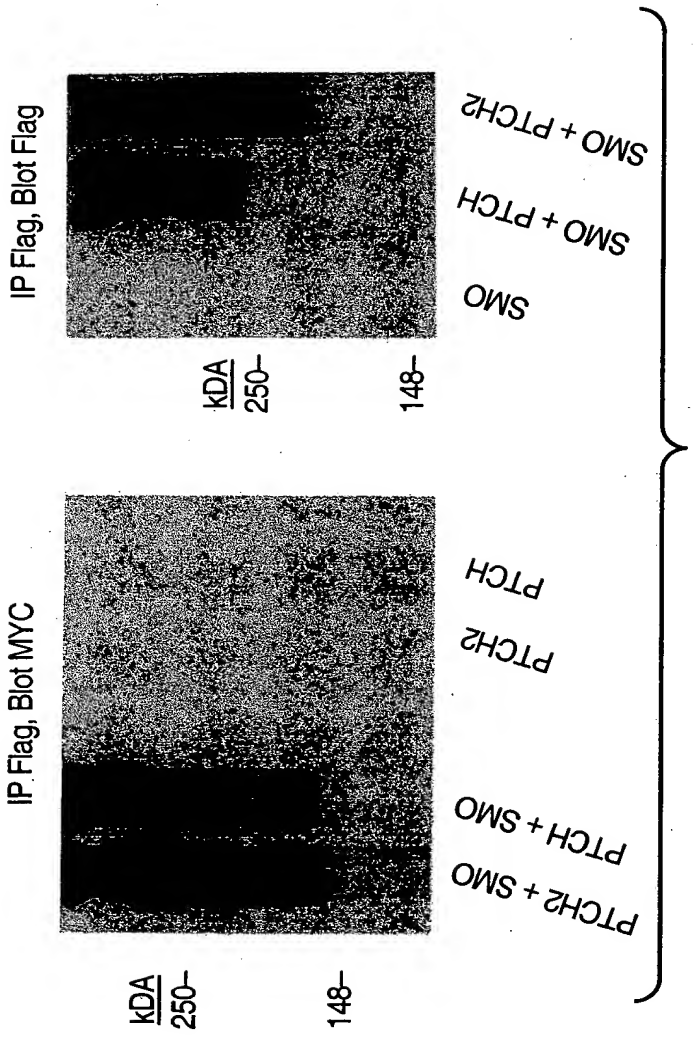
IP Flag, Blot Flag
kDA
250
148
SMO
SMO + PTCH
SMO + PTCH2
IP Flag, Blot MYC
kDA
250
148
PTCH
PTCH2
PTCH + SMO
PTCH2 + SMO

FIG._7B

```
                  10         20         30         40         50
hPtch-2   MTRSPPLRELPPSYTPPARTAAPQILAGSLKAPLWLRAYFQGLLFSLGCG
          * *. .* ***********..**.******.******************
mPatched2 MVRPLSLGELPPSYTPPARSSAPHILAGSLQAPLWLRAYFQGLLFSLGCR
                  10         20         30         40         50

                  60         70         80         90         100
hPtch-2   IQRHCGKVLFLGLLAFGALALGLRMAIIETNLEQLWVEVGSRVSQELHYT
          **.**********.**********.*.***.******************
mPatched2 IQKHCGKVLFLGLVAFGALALGLRVAVIETDLEQLWVEVGSRVSQELHYT
                  60         70         80         90         100

                 110        120        130        140        150
hPtch-2   KEKLGEEAAYTSQMLIQTARQEGENILTPEALGLHLQAALTASKVQVSLY
          ******************.*** *.******.*****************
mPatched2 KEKLGEEAAYTSQMLIQTAHQEGGNVLTPEALDLHLQAALTASKVQVSLY
                 110        120        130        140        150

                 160        170        180        190        200
hPtch-2   GKSWDLNKICYKSGVPLIENGMIEWMIEKLFPCVILTPLDCFWEGAKLQG
          ************************.************************
mPatched2 GKSWDLNKICYKSGVPLIENGMIERMIEKLFPCVILTPLDCFWEGAKLQG
                 160        170        180        190        200

                 210        220        230        240        250
hPtch-2   GSAYLPGRPDIQWTNLDPEQLLEELGPFASLEGFRELLDKAQVGQAYVGR
          ******************.*********************************
mPatched2 GSAYLPGRPDIQWTNLDPQQLLEELGPFASLEGFRELLDKAQVGQAYVGR
                 210        220        230        240        250

                 260        270        280        290        300
hPtch-2   PCLHPDDLHCPPSAPNHHSRQAPNVAHELSGGCHGFSHKFMHWQEELLLG
          ***.*** ********.*********.************************
mPatched2 PCLDPDDPHCPPSAPNRHSRQAPNVAQELSGGCHGFSHKFMHWQEELLLG
                 260        270        280        290        300

                 310        320        330        340        350
hPtch-2   GMARDPQGELLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQAST
          * *** **.****************************************
mPatched2 GTARDLQGQLLRAEALQSTFLLMSPRQLYEHFRGDYQTHDIGWSEEQASM
                 310        320        330        340        350
```

FIG._8A

```
                360        370        380        390        400
hPtch-2   VLQAWQRRFVQLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVG
          ****************** ******************.******..****
mPatched2 VLQAWQRRFVQLAQEALPANASQQIHAFSSTTLDDILRAFSEVSTTRVVG
                360        370        380        390        400

                410        420        430        440        450
hPtch-2   GYLLMLAYACVTMLRWDCAQSQGSVGLAGVLLVALAVASGLGLCALLGIT
          ***********************.****************************
mPatched2 GYLLMLAYACVTMLRWDCAQSQGAVGLAGVLLVALAVASGLGLCALLGIT
                410        420        430        440        450

                460        470        480        490        500
hPtch-2   FNAATTQVLPFLALGIGVDDVFLLAHAFTEALPGTPLQERMGECLQRTGT
          ********************.******** * *.*** *******. ***
mPatched2 FNAATTQVLPFLALGIGVDDIFLLAHAFTKAPPDTPLPERMGECLRSTGT
                460        470        480        490        500

                510        520        530        540        550
hPtch-2   SVVLTSINNMAAFLMAALVPIPALRAFSLQAAIVVGCTFVAVMLVFPAIL
          ** ***.*** **.************************ * **********
mPatched2 SVALTSVNNMVAFFMAALVPIPALRAFSLQAAIVVGCNFAAVMLVFPAIL
                510        520        530        540        550

                560        570        580        590        600
hPtch-2   SLDLRRRHCQRLDVLCCFSSPCSAQVIQILPQELGDGTVPVGIAHLTATV
          ******** ********************.******* .************
mPatched2 SLDLRRRHRQRLDVLCCFSSPCSAQVIQMLPQELGDRAVPVGIAHLTATV
                560        570        580        590        600

                610        620        630        640        650
hPtch-2   QAFTHCEASSQHVVTILPPQAHLVPPPSDPLGSELFSPGGSTRDLLGQEE
          ************************..*.********.**********.***
mPatched2 QAFTHCEASSQHVVTILPPQAHLLSPASDPLGSELYSPGGSTRDLLSQEE
                610        620        630        640        650

                660        670        680        690        700
hPtch-2   ETRQKAACKSLPCARWNLAHFARYQFAPLLLQSHAKAIVLVLFGALLGLS
          *  .***..* **.* ****************..***.**..********
mPatched2 GTGPQAACRPLLCAHWTLAHFARYQFAPLLLQTRAKALVLLFFGALLGLS
                660        670        680        690        700
```

FIG._8B

```
                710        720        730        740        750
hPtch-2    LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA
           **************************************************
mPatched2  LYGATLVQDGLALTDVVPRGTKEHAFLSAQLRYFSLYEVALVTQGGFDYA
                710        720        730        740        750

                760        770        780        790        800
hPtch-2    HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRNWLQGIQAAFDQDW
           ************************************.*************
mPatched2  HSQRALFDLHQRFSSLKAVLPPPATQAPRTWLHYYRSWLQGIQAAFDQDW
                760        770        780        790        800

                810        820        830        840        850
hPtch-2    ASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPLDFSQLTTRKLVDREGL
           ****** ********************.*****************.***
mPatched2  ASGRITCHSYRNGSEDGALAYKLLIQTGNAQEPLDFSQLTTRKLVDKEGL
                810        820        830        840        850

                860        870        880        890        900
hPtch-2    IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP
           **************************************************
mPatched2  IPPELFYMGLTVWVSSDPLGLAASQANFYPPPPEWLHDKYDTTGENLRIP
                860        870        880        890        900

                910        920        930        940        950
hPtch-2    PAQPLEFAQFPFLLRGLQKTADFVEAIEGARAACAEAGQAGVHAYPSGSP
           .*************.******************.***************
mPatched2  AAQPLEFAQFPFLLHGLQKTADFVEAIEGARAACTEAGQAGVHAYPSGSP
                910        920        930        940        950

                960        970        980        990       1000
hPtch-2    FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLNPWTAGLIVLVLAMMT
           ***********************************.***************
mPatched2  FLFWEQYLGLRRCFLLAVCILLVCTFLVCALLLLSPWTAGLIVLVLAMMT
                960        970        980        990       1000

               1010       1020       1030       1040       1050
hPtch-2    VELFGIMGFLGIKLSAIPVVILVASVGIGVEFTVHVALGFLTTQGSRNLR
           *************************.****************..******
mPatched2  VELFGIMGFLGIKLSAIPVVILVASIGIGVEFTVHVALGFLTSHGSRNLR
               1010       1020       1030       1040       1050
```

FIG._8C

```
                1060       1070       1080       1090       1100
hPtch-2         AAHALEHTFAPVTDGAISTLLGLLMLAGSHFDFIVRYFFAALTVLTLLGL
                ** ***.*********.***********.****.****  *********
mPatched2       AASALEQTFAPVTDGAVSTLLGLLMLAGSNFDFIIRYFFVVLTVLTLLGL
                1060       1070       1080       1090       1100

                1110       1120       1130       1140       1150
hPtch-2         LHGLVLLPVLLSILGPPPEVIQMYKESPEILSPPAPQGGGLRWGASSSLP
                ****.*************.*.*.*****. *...*** *****. ...**
mPatched2       LHGLLLLPVLLSILGPPPQVVQVYKESPQTLNSAAPQRGGLRWDRPPTLP
                1110       1120       1130       1140       1150

                1160       1170       1180       1190       1200
hPtch-2         QSFARVTTSMTVAIHPPPLPGAYIHPAPDEPPWSPAATSSGNLSSRGPGP
                ************.*********.***..**
mPatched2       QSFARVTTSMTVALHPPPLPGAYVHPASEEPT
                1160       1170       1180

hPtch-2         ATG
```

FIG._8D

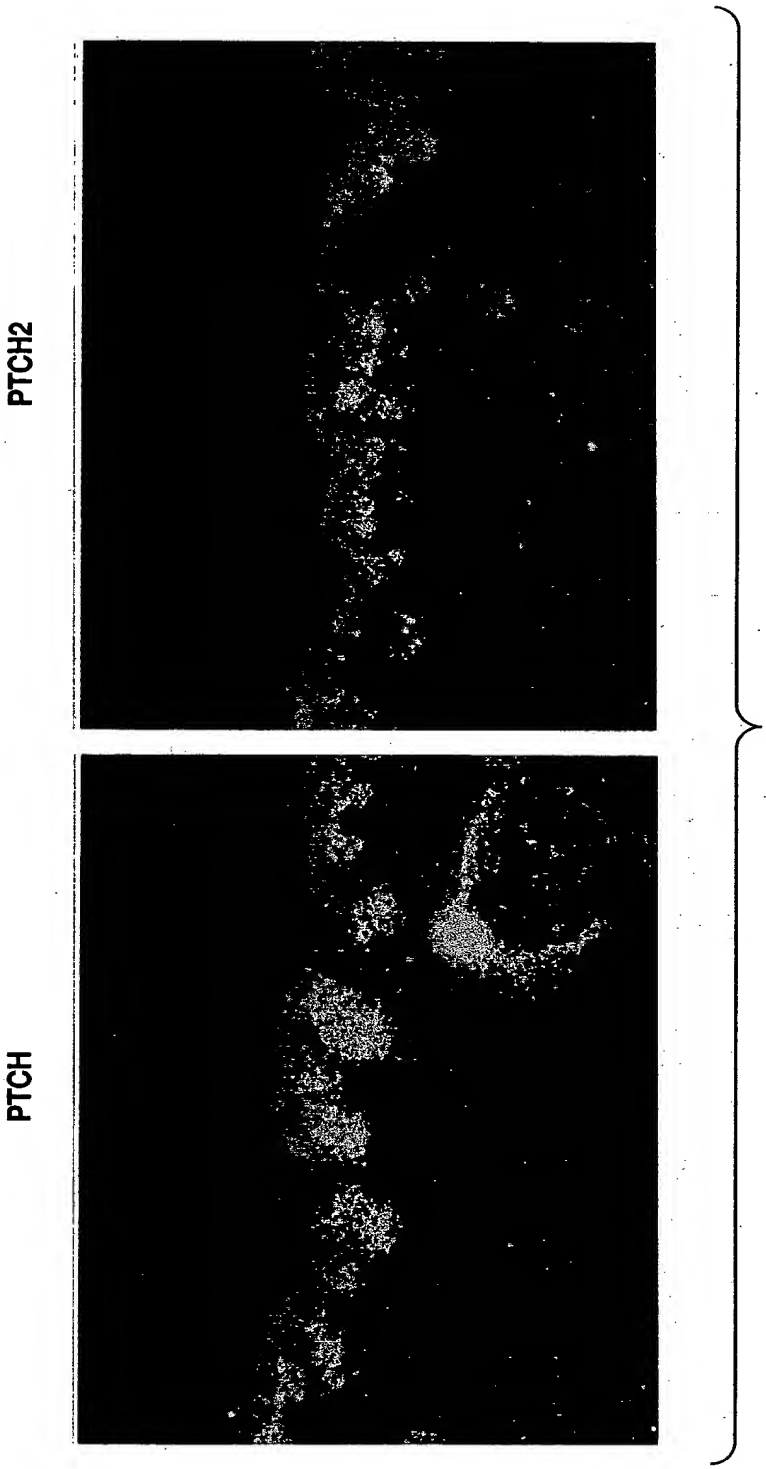

FIG._9

```
  1 CCCACGCGTC CGGGAGAAGC TGGGGGAGGA GGCTGCATAC ACCTCTCAGA TGCTGATACA GACCGCACGC CAGGAGGGAG AGAACATCCT CACACCCGAA
    GGGTGCGCAG GCCCTCTTCG ACCCCCTCCT CCGACGTATG TGGAGAGTCT ACGACTATGT CTGGCGTGCG GTCCTCCCTC TCTTGTAGGA GTGTGGGCTT

101 GCACTTGGCC TCCACCTCCA GGCAGCCCTC ACTGCCAGTA AAGTCCAAGT ATCACTCTAT GGGAAGTCCT GGGATTTGAA CAAAATCTGC TACAAGTCAG
    CGTGAACCGG AGGTGGAGGT CCGTCGGGAG TGACGGTCAT TTCAGGTTCA TAGTGAGATA CCCTTCAGGA CCCTAAACTT GTTTTAGACG ATGTTCAGTC

201 GAGTTCCCCT TATTGAAAAT GGAATGATTG AGCGGATGAT TGAGAAGCTG TTTCCGTGCG TGATCCTCAC CCCCCTCGAC TGCTTCTGGG AGGGAGCCAA
    CTCAAGGGGA ATAACTTTTA CCTTACTAAC TCGCCTACTA ACTCTTCGAC AAAGGCACGC ACTAGGAGTG GGGGGAGCTG ACGAAGACCC TCCCTCGGTT

301 ACTCCAAGGG GGCTCCGCCT ACCTGCCGCT CCCAATGTGG CTCACGAGCT GAGTGGGGGC TGCCATGGCT TCTCCCACAA ATTCATGCAC TGGCAGGAGG
    TGAGGTTCCC CCGAGGCGGA TGGACGGCGA GGGTTACACC GAGTGCTCGA CTCACCCCCG ACGGTACCGA AGAGGGTGTT TAAGTACGTG ACCGTCCTCC

401 AATTGCTGCT GGGAGGCATG GCCAGAGACC CCCAAGGAGA GCTGCTGAGG GCAGAGGCCC TGCAGAGCAC CTTCTTGCTG ATGAGTCCCC GCCAGCTGTA
    TTAACGACGA CCCTCCGTAC CGGTCTCTGG GGGTTCCTCT CGACGACTCC CGTCTCCGGG ACGTCTCGTG GAAGAACGAC TACTCAGGGG CGGTCGACAT

501 CGAGCATTTC CGGGGTGACT ATCAGACACA TGACATTGGC TGGAGTGAGG AGCAGGCCAG CACAGTGCTA CAAGCCTGGC AGCGGCGCTT TGTGCAGGTC
    GCTCGTAAAG GCCCCACTGA TAGTCTGTGT ACTGTAACCG ACCTCACTCC TCGTCCGGTC GTGTCACGAT GTTCGGACCG TCGCCGCGAA ACACGTCCAG

601 GGTATGGACA AGGACAGGGG GGTGCCCTGA GGCCATTCCC TCCTCCTGCC CCCTCCTATC CACCCTGTTT CTCCAGCTGG CCCAGGAGGC CCTGCCTGAG
    CCATACCTGT TCCTGTCCCC CCACGGGACT CCGGTAAGGG AGGAGGACGG GGGAGGATAG GTGGGACAAA GAGGTCGACC GGGTCCTCCG GGACGGACTC
```

FIG._10A

```
701 AACGCTTCCC AGCAGATCCA TGCCTTCTCC TCCACCACCC TGGATGACAT CCTGCATGCG TTCTCTGAAG TCAGTGCTGC CCGTGTGGTG GGAGGCTATC
    TTGCGAAGGG TCGTCTAGGT ACGGAAGAGG AGGTGGTGGG ACCTACTGTA GGACGTACGC AAGAGACTTC AGTCACGACG GGCACACCAC CCTCCGATAG

801 TGCTCATGGT GGGTCTTGCA CCTGGCACCT TGCCCCCACC CCACCTCCAA CCAGTGCCCA CCCTGGGGAG CCCCTGAGAC TGCCCTTTCC CCCCACAGCT
    ACGAGTACCA CCCAGAACGT GGACCGTGGA ACGGGGGTGG GGTGGAGGTT GGTCACGGGT GGGACCCCTC GGGGACTCTG ACGGGAAAGG GGGGTGTCGA

901 GGCCTATGCC TGTGTGACCA TGCTGCGGTG GGACTGCGCC CAGTCCCAGG GTTCCGTGGG CCTTGCCGGG GTACTGCTGG TGGCCCTGGC GGTGGCCTCA
    CCGGATACGG ACACACTGGT ACGACGCCAC CCTGACGCGG GTCAGGGTCC CAAGGCACCC GGAACGGCCC CATGACGACC ACCGGGACCG CCACCGGAGT

1001 GGCCTTGGGC TCTGTGCCCT GCTCGGCATC ACCTTCAATG CTGCCACTAC CCAGGTACGC CAGGACTGCA GGGCAGACTC AGTGCCAGTC ACCAGGCTTC
     CCGGAACCCG AGACACGGGA CGAGCCGTAG TGGAAGTTAC GACGGTGATG GGTCCATGCG GTCCTGACGT CCCGTCTGAG TCACGGTCAG TGGTCCGAAG

1101 ACGGGTCCTC AGCTGCCCGC TCCTCTGCCC CTCCAGGTGC TGCCCTTCTT GACTCTGGGA ATCGGCGTGG ATGACGTATT CCTGCTGGCG CATGCCTTCA
     TGCCCAGGAG TCGACGGGCG AGGAGACGGG GAGGTCCACG ACGGGAAGAA CTGAGACCCT TAGCCGCACC TACTGCATAA GGACGACCGC GTACGGAAGT

1201 CAGAGGCTCT GCCTGGCACC CCTCTCCAGG TGGGGCCTTG TCCCCCAGGG CTCATCTGAG GCAGCTCAGC TTACTGGTTA AGAGCCTCTT GGTTCAAGTG
     GTCTCCGAGA CGGACCGTGG GGAGAGGTCC ACCCCGGAAC AGGGGGTCCC GAGTAGACTC CGTCGAGTCG AATGACCAAT TCTCGGAGAA CCAAGTTCAC

1301 ACCTTGGGCT GCTAATGAAC CTCGGTGCCT CTTGTCCCCA TGTGTAAACA GGGGAAATAA TAGTGCTGTG TCCTAAGGGT TATTGTTTGG ATCAGTGAAG
     TGGAACCCGA CGATTACTTG GAGCCACGGA GAACAGGGGT ACACATTTGT CCCCTTTATT ATCACGACAC AGGATTCCCA ATAACAAACC TAGTCACTTC

1401 TAACTCAAGT TGAATGCTTA GAACAGCCCA TCATACGTAC ATGGTACCCA ATAAATGCTA GCCACTGTGT TATGACTGCC CCACCTCTGC ACCCCAAGTT
     ATTGAGTTCA ACTTACGAAT CTTGTCGGGT AGTATGCATG TACCATGGGT TATTTACGAT CGGTGACACA ATACTGACGG GGTGGAGACG TGGGGTTCAA
```

FIG._10B

```
1501 CCTGAGCCTC CCCTTCACTC CACTTTGACA CGGCCCCTCC CTTGTGACCT GAGGGCAGGT CCCCACTCTG TCCTGGCAGG AGCGCATGGG CGAGTGTCTG
     GGACTCGGAG GGGAAGTGAG GTGAAACTGT GCCGGGGAGG GAACACTGGA CTCCCGTCCA GGGGTGAGAC AGGACCGTCC TCGCGTACCC GCTCACAGAC

1601 CAGCGCACGG GCACCAGTGT TGTACTCACA TCCATCAACA ACATGGCCGC CTTCCTCATG GCTGCCCTCG TTCCCATCCC TGCGCTGCGA GCCTTCTCCC
     GTCGCGTGCC CGTGGTCACA ACATGAGTGT AGGTAGTTGT TGTACCGGCG GAAGGAGTAC CGACGGGAGC AAGGGTAGGG ACGCGACGCT CGGAAGAGGG

1701 TACAGCCTGG ACCTACGGCG GCGCCACTGC CAGCGCCTTG ATGTGCTCTG CTGCTTCTCC AGGTACTGCC TGCGCCCCAG CCCCTTCCTC CCGTGACCCA
     ATGTCGGACC TGGATGCCGC CGCGGTGACG GTCGCGGAAC TACACGAGAC GACGAAGAGG TCCATGACGG ACGCGGGGTC GGGGAAGGAG GGCACTGGGT

1801 CGCCAGCCTG TCCCCTCACC AGCATTTCAA GGCACAGACC TGTCATCCAC TCTCTACCTC TTCCAGTCCC TGCTCTGCTC AGGTGATTCA GATCCTGCCC
     GCGGTCGGAC AGGGGAGTGG TCGTAAAGTT CCGTGTCTGG ACAGTAGGTG AGAGATGGAG AAGGTCAGGG ACGAGACGAG TCCACTAAGT CTAGGACGGG

1901 CAGGAGCTGG GGGACGGGAC AGTACCAGTG GGCATTGCCC ACCTCACTGC CACAGTTCAA GCCTTTACCC ACTGTGAAGC CAGCAGCCAG CATGTGGTCA
     GTCCTCGACC CCCTGCCCTG TCATGGTCAC CCGTAACGGG TGGAGTGACG GTGTCAAGTT CGGAAATGGG TGACACTTCG GTCGTCGGTC GTACACCAGT

2001 CCATCCTGCC TCCCCAAGCC CACCTGGTGC CCCCACCTTC TGACCCACTG GGCTCTGAGC TCTTCAGCCC TGGAGGGTCC ACACGGGACC TTCTAGGCCA
     GGTAGGACGG AGGGGTTCGG GTGGACCACG GGGGTGGAAG ACTGGGTGAC CCGAGACTCG AGAAGTCGGG ACCTCCCAGG TGTGCCCTGG AAGATCCGGT

2101 GGAGGAGGAG ACAAGGCAGA AGGCAGCCTG CAAGTCCCTG CCCTGTGCCC GCTGGAATCT TGCCCATTTC GCCCGCTATC AGTTTGCCCC GTTGCTGCTC
     CCTCCTCCTC TGTTCCGTCT TCCGTCGGAC GTTCAGGGAC GGGACACGGG CGACCTTAGA ACGGGTAAAG CGGGCGATAG TCAAACGGGG CAACGACGAG

2201 CAGTCACATG CCAAGGCCAT CGTGCTGGTG CTCTTTGGTG CTCTTCTGGG CCTGAGCCTC TACGGAGCCA CCTTGGTGCA AGACGGCCTG GCCCTGACGG
     GTCAGTGTAC GGTTCCGGTA GCACGACCAC GAGAAACCAC GAGAAGACCC GGACTCGGAG ATGCCTCGGT GGAACCACGT TCTGCCGGAC CGGGACTGCC
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FIG._10C

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2301 ATGTGGTGCC TCGGGGCACC AAGGAGCATG CCTTCCTGAG CGCCCAGCTC AGGTACTTCT CCCTGTACGA GGTGGCCCTG GTGACCCAGG GTGGCTTTGA
     TACACCACGG AGCCCCGTGG TTCCTCGTAC GGAAGGACTC GCGGGTCGAG TCCATGAAGA GGGACATGCT CCACCGGGAC CACTGGGTCC CACCGAAACT

2401 CTACGCCCAC TCCCAACGCG CCCTCTTTGA TCTGCACCAG CGCTTCAGTT CCCTCAAGGC GGTGCTGCCC CCACCGGCCA CCCAGGCACC CCGCACCTGG
     GATGCGGGTG AGGGTTGCGC GGGAGAAACT AGACGTGGTC GCGAAGTCAA GGGAGTTCCG CCACGACGGG GGTGGCCGGT GGGTCCGTGG GGCGTGGACC

2501 CTGCACTATT ACCGCAACTG GCTACAGGGA ATCCAGGCTG CCTTTGACCA GGACTGGGCT TCTGGGCGCA TCACCCGCCA CTCGTACCGC AATGGCTCTG
     GACGTGATAA TGGCGTTGAC CGATGTCCCT TAGGTCCGAC GGAAACTGGT CCTGACCCGA AGACCCGCGT AGTGGGCGGT GAGCATGGCG TTACCGAGAC

2601 AGGATGGGGC CCTGGCCTAC AAGCTGCTCA TCCAGACTGG AGACGCCCAG GAGCCTCTGG ATTTCAGCCA GGTTGGGAGA GGGCTGGAGG GGTCCACTAG
     TCCTACCCCG GGACCGGATG TTCGACGAGT AGGTCTGACC TCTGCGGGTC CTCGGAGACC TAAAGTCGGT CCAACCCTCT CCCGACCTCC CCAGGTGATC

2701 TACAGGGGCT GCAGGCCTCC TGGGCCCAGG CCTTCAGCCC TCTCTGCCTC TGCAGCTGAC CACAAGGAAG CTGGTGGACA GAGAGGGACT GATTCCACCC
     ATGTCCCCGA CGTCCGGAGG ACCCGGGTCC GGAAGTCGGG AGAGACGGAG ACGTCGACTG GTGTTCCTTC GACCACCTGT CTCTCCCTGA CTAAGGTGGG

2801 GAGCTCTTCT ACATGGGGCT GACCGTGTGG GTGAGCAGTG ACCCCCTGGG TCTGGCAGCC TCACAGGCCA ACTTCTACCC CCCACCTCCT GAATGGCTGC
     CTCGAGAAGA TGTACCCCGA CTGGCACACC CACTCGTCAC TGGGGGACCC AGACCGTCGG AGTGTCCGGT TGAAGATGGG GGGTGGAGGA CTTACCGACG

2901 ACGACAAATA CGACACCACG GGGGAGAACC TTCGCAGTGA GTCTTGGGGG GAGCTCGGCA AGAGCCTCAG CCTCGCCCAC ACAAGCCCTG AGCCTGAGGC
     TGCTGTTTAT GCTGTGGTGC CCCCTCTTGG AAGCGTCACT CAGAACCCCC CTCGAGCCGT TCTCGGAGTC GGAGCGGGTG TGTTCGGGAC TCGGACTCCG

3001 CCTGCCCACT CTGCCCCGTG CTCACCGCCC TGTCCCTCTC CCTCTTCTCC CTTCCCCTCC CCTCCACAGT CCCGCCAGCT CAGCCCTTGG AGTTTGCCCA
     GGACGGGTGA GACGGGGCAC GAGTGGCGGG ACAGGGAGAG GGAGAAGAGG GAAGGGGAGG GGAGGTGTCA GGGCGGTCGA GTCGGGAACC TCAAACGGGT
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FIG._10D

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3101 GTTCCCCTTC CTGCTGCGTG GCCTCCAGAA GACTGCAGAC TTTGTGGAGG CCATCGAGGG GGCCCGGGCA GCATGCGCAG AGGCCGGCCA GGCTGGGGTG
     CAAGGGGAAG GACGACGCAC CGGAGGTCTT CTGACGTCTG AAACACCTCC GGTAGCTCCC CCGGGCCCGT CGTACGCGTC TCCGGCCGGT CCGACCCCAC

3201 CACGCCTACC CCAGCGGCTC CCCCTTCCTC TTCTGGGAAC AGTATCTGGG CCTGCGGCGC TGCTTCCTGC TGGCCGTCTG CATCCTGCTG GTGTGCACTT
     GTGCGGATGG GGTCGCCGAG GGGGAAGGAG AAGACCCTTG TCATAGACCC GGACGCCGCG ACGAAGGACG ACCGGCAGAC GTAGGACGAC CACACGTGAA

3301 TCCTCGTCTG TGCTCTGCTG CTCCTCAACC CCTGGACGGC TGGCCTCATA GTGAGTGCTT GCAGGAGTGG GGACAGAGAC ACCCCACCCT TCCCTGCCCA
     AGGAGCAGAC ACGAGACGAC GAGGAGTTGG GGACCTGCCG ACCGGAGTAT CACTCACGAA CGTCCTCACC CCTGTCTCTG TGGGGTGGGA AGGGACGGGT

3401 GCCTGTCATC CCTCCTGCCA GGAGCCCTCT GTGAGCCCTG TCTCCCTCAG GTGCTGGTCC TGGCGATGAT GACAGTGGAA CTCTTTGGTA TCATGGGTTT
     CGGACAGTAG GGAGGACGGT CCTCGGGAGA CACTCGGGAC AGAGGGAGTC CACGACCAGG ACCGCTACTA CTGTCACCTT GAGAAACCAT AGTACCCAAA

3501 CCTGGGCATC AAGCTGAGTG CCATCCCCGT GGTGATCCTT GTGGCCTCTG TAGGCATTGG CGTTGAGTTC ACAGTCCACG TGGCTCTGGT GAGCACGGGC
     GGACCCGTAG TTCGACTCAC GGTAGGGGCA CCACTAGGAA CACCGGAGAC ATCCGTAACC GCAACTCAAG TGTCAGGTGC ACCGAGACCA CTCGTGCCCG

3601 ACCCCGGGGA GGGACCAATC AGCTGATTCA GTATTCAACA CATATTGTTC AAGCCCCTAC TATGTGCTAG GTACTATTTA AGAATTTGGG CTGGGTGGAC
     TGGGGCCCCT CCCTGGTTAG TCGACTAAGT CATAAGTTGT GTATAACAAG TTCGGGGATG ATACACGATC CATGATAAAT TCTTAAACCC GACCCACCTG

3701 GTGGTGGCTC ATTCCTGTAA TCCCAGCACT TTGGGAGGCC GAGGCGGGTG GATCACCTGA GGTCGGGAGT TCGAAACCAG CCTGGCCAAC ATGGTGAAAC
     CACCACCGAG TAAGGACATT AGGGTCGTGA AACCCTCCGG CTCCGCCCAC CTAGTGGACT CCAGCCCTCA AGCTTTGGTC GGACCGGTTG TACCACTTTG

3801 CCTGTCTTTA CTAAAAATAC AAAAAATTAG CCAGGCGTGG TGGCACATGC CAGTAGTCCC AGCTACTTTG GAGGCTGAGG CAGAATTGCT TGAACCTGGG
     GGACAGAAAT GATTTTTATG TTTTTTAATC GGTCCGCACC ACCGTGTACG GTCATCAGGG TCGATGAAAC CTCCGACTCC GTCTTAACGA ACTTGGACCC

3901 AGGCGAAGGT TGCAGTGAGC TGAGATCGTG CCATTGCACT CCAGCCTGGG CAACAAGAGT GCAACTCTCC GTCTCAAAAA AAAAAAAAAA AAGGGCGGCC
     TCCGCTTCCA ACGTCACTCG ACTCTAGCAC GGTAACGTGA GGTCGGACCC GTTGTTCTCA CGTTGAGAGG CAGAGTTTTT TTTTTTTTTT TTCCCGCCGG

4001 GCGA
     CGCT
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FIG._10E

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  1 TTCCGGCATG ACTCGATCGC CGCCCCTCAG AGAGCTGCCC CCGAGTTACA CACCCCCAGC TCGAACCGCA GCACCCCAGA TCCTAGCTGG GAGCCTGAAG
    AAGGCCGTAC TGAGCTAGCG GCGGGGAGTC TCTCGACGGG GGCTCAATGT GTGGGGGTCG AGCTTGGCGT CGTGGGGTCT AGGATCGACC CTCGGACTTC

101 GCTCCACTCT GGCTTCGTGC TTACTTCCAG GGCCTGCTCT TCTCTCTGGG ATGCGGGATC CAGAGACATT GTGGCAAAGT GCTCTTTCTG GGACTGTTGG
    CGAGGTGAGA CCGAAGCACG AATGAAGGTC CCGGACGAGA AGAGAGACCC TACGCCCTAG GTCTCTGTAA CACCGTTTCA CGAGAAAGAC CCTGACAACC

201 CCTTTGGGGC CCTGGCATTA GGTCTCCGCA TGGCCATTAT TGAGACAAAC TTGGAACAGC TCTGGGTAGA AGTGGGCAGC CGGGTGAGCC AGGAGCTGCA
    GGAAACCCCG GGACCGTAAT CCAGAGGCGT ACCGGTAATA ACTCTGTTTG AACCTTGTCG AGACCCATCT TCACCCGTCG GCCCACTCGG TCCTCGACGT

301 TTACACCAAG GAGAAGCTGG GGGAGGAGGC TGCATACACC TCTCAGATGC TGATACAGAC CGCACGCCAG GAGGGAGAGA ACATCCTCAC ACCCGAAGCA
    AATGTGGTTC CTCTTCGACC CCCTCCTCCG ACGTATGTGG AGAGTCTACG ACTATGTCTG GCGTGCGGTC CTCCCTCTCT TGTAGGAGTG TGGGCTTCGT

401 CTTGGCCTCC ACCTCCAGGC AGCCCTCACT GCCAGTAAAG TCCAAGTATC ACTCTATGGG AAGTCCTGGG ATTTGAACAA AATCTGCTAC AAGTCAGGAG
    GAACCGGAGG TGGAGGTCCG TCGGGAGTGA CGGTCATTTC AGGTTCATAG TGAGATACCC TTCAGGACCC TAAACTTGTT TTAGACGATG TTCAGTCCTC

501 TTCCCCTTAT TGAAAATGGA ATGATTGAGT GGATGATTGA GAAGCTGTTT CCGTGCGTGA TCCTCACCCC CCTCGACTGC TTCTGGGAGG GAGCCAAACT
    AAGGGGAATA ACTTTTACCT TACTAACTCA CCTACTAACT CTTCGACAAA GGCACGCACT AGGAGTGGGG GGAGCTGACG AAGACCCTCC CTCGGTTTGA
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FIG._11A

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601 CCAAGGGGGC TCCGCCTACC TGCCCGGCCG CCCGGATATC CAGTGGACCA ACCTGGATCC AGAGCAGCTG CTGGAGGAGC TGGGTCCCTT TGCCTCCCTT
    GGTTCCCCCG AGGCGGATGG ACGGGCCGGC GGGCCTATAG GTCACCTGGT TGGACCTAGG TCTCGTCGAC GACCTCCTCG ACCCAGGGAA ACGGAGGGAA

701 GAGGGCTTCC GGGAGCTGCT AGACAAGGCA CAGGTGGGCC AGGCCTACGT GGGGCGGCCC TGTCTGCACC CTGATGACCT CCACTGCCCA CCTAGTGCCC
    CTCCCGAAGG CCCTCGACGA TCTGTTCCGT GTCCACCCGG TCCGGATGCA CCCCGCCGGG ACAGACGTGG GACTACTGGA GGTGACGGGT GGATCACGGG

801 CCAACCATCA CAGCAGGCAG GCTCCCAATG TGGCTCACGA GCTGAGTGGG GGCTGCCATG GCTTCTCCCA CAAATTCATG CACTGGCAGG AGGAATTGCT
    GGTTGGTAGT GTCGTCCGTC CGAGGGTTAC ACCGAGTGCT CGACTCACCC CCGACGGTAC CGAAGAGGGT GTTTAAGTAC GTGACCGTCC TCCTTAACGA

901 GCTGGGAGGC ATGGCCAGAG ACCCCCAAGG AGAGCTGCTG AGGGCAGAGG CCCTGCAGAG CACCTTCTTG CTGATGAGTC CCCGCCAGCT GTACGAGCAT
    CGACCCTCCG TACCGGTCTC TGGGGGTTCC TCTCGACGAC TCCCGTCTCC GGGACGTCTC GTGGAAGAAC GACTACTCAG GGGCGGTCGA CATGCTCGTA

1001 TTCCGGGGTG ACTATCAGAC ACATGACATT GGCTGGAGTG AGGAGCAGGC CAGCACAGTG CTACAAGCCT GGCAGCGGCG CTTTGTGCAG CTGGCCCAGG
     AAGGCCCCAC TGATAGTCTG TGTACTGTAA CCGACCTCAC TCCTCGTCCG GTCGTGTCAC GATGTTCGGA CCGTCGCCGC GAAACACGTC GACCGGGTCC

1101 AGGCCCTGCC TGAGAACGCT TCCCAGCAGA TCCATGCCTT CTCCTCCACC ACCCTGGATA ACATCCTGCA TGCGTTCTCT GAAGTCAGTG CTGCCCGTGT
     TCCGGGACGG ACTCTTGCGA AGGGTCGTCT AGGTACGGAA GAGGAGGTGG TGGGACCTAT TGTAGGACGT ACGCAAGAGA CTTCAGTCAC GACGGGCACA

1201 GGTGGGAGGC TATCTGCTCA TGCTGGCCTA TGCCTGTGTG ACCATGCTGC GGTGGGACTG CGCCCAGTCC CAGGGTTCCG TGGGCCTTGC CGGGGTACTG
     CCACCCTCCG ATAGACGAGT ACGACCGGAT ACGGACACAC TGGTACGACG CCACCCTGAC GCGGGTCAGG GTCCCAAGGC ACCCGGAACG GCCCCATGAC

1301 CTGGTGGCCC TGGCGGTGGC CTCAGGCCTT GGGCTCTGTG CCCTGCTCGG CATCACCTTC AATGCTGCCA CTACCCAGGT GCTGCCCTTC TTGGCTCTGG
     GACCACCGGG ACCGCCACCG GAGTCCGGAA CCCGAGACAC GGGACGAGCC GTAGTGGAAG TTACGACGGT GATGGGTCCA CGACGGGAAG AACCGAGACC
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FIG._11B

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1401 GAATCGGCGT GGATGACGTA TTCCTGCTGG CGCATGCCTT CACAGAGGCT CTGCCTGGCA CCCCTCTCCA GGAGCGCATG GGCGAGTGTC TGCAGCGCAC
     CTTAGCCGCA CCTACTGCAT AAGGACGACC GCGTACGGAA GTGTCTCCGA GACGGACCGT GGGGAGAGGT CCTCGCGTAC CCGCTCACAG ACGTCGCGTG

1501 GGGCACCAGT GTCGTACTCA CATCCATCAA CAACATGGCC GCCTTCCTCA TGGCTGCCCT CGTTCCCATC CCTGCGCTGC GAGCCTTCTC CTTACAGCCA
     CCCGTGGTCA CAGCATGAGT GTAGGTAGTT GTTGTACCGG CGGAAGGAGT ACCGACGGGA GCAAGGGTAG GGACGCGACG CTCGGAAGAG GAATGTCGGT

1601 TCCTCAGCCT GGACCTACGG CGGCGCCACT GCCAGCGCCT TGATGTGCTC TGCTGCTTCT CCAGTCCCTG CTCTGCTCAG GTGATTCAGA TCCTGCCCCA
     AGGAGTCGGA CCTGGATGCC GCCGCGGTGA CGGTCGCGGA ACTACACGAG ACGACGAAGA GGTCAGGGAC GAGACGAGTC CACTAAGTCT AGGACGGGGT

1701 GGAGCTGGGG GACGGGACAG TACCAGTGGG CATTGCCCAC CTCACTGCCA CAGTTCAAGC CTTTACCCAC TGTGAAGCCA GCAGCCAGCA TGTGGTCACC
     CCTCGACCCC CTGCCCTGTC ATGGTCACCC GTAACGGGTG GAGTGACGGT GTCAAGTTCG GAAATGGGTG ACACTTCGGT CGTCGGTCGT ACACCAGTGG

1801 ATCCTGCCTC CCCAAGCCCA CCTGGTGCCC CCACCTTCTG ACCCACTGGG CTCTGAGCTC TTCAGCCCTG GAGGGTCCAC ACGGGACCTT CTAGGCCAGG
     TAGGACGGAG GGGTTCGGGT GGACCACGGG GGTGGAAGAC TGGGTGACCC GAGACTCGAG AAGTCGGGAC CTCCCAGGTG TGCCCTGGAA GATCCGGTCC

1901 AGGAGGAGAC AAGGCAGAAG GCAGCCTGCA AGTCCCTGCC CTGTGCCCGC TGGAATCTTG CCCATTTCGC CCCGGAATTC CTGCAGCCCG GGGGATCCAC
     TCCTCCTCTG TTCCGTCTTC CGTCGGACGT TCAGGGACGG GACACGGGCG ACCTTAGAAC GGGTAAAGCG GGGCCTTAAG GACGTCGGGC CCCCTAGGTG

2001 TAGTTCTAGA GCGGCCGCCA CCGCGGTGGA GCTCCAGCTT TTGTTCCCTT TAGTGAGGGT TAATTGCGCG CTTGGGTATC TT
     ATCAAGATCT CGCCGGCGGT GGCGCCACCT CGAGGTCGAA AACAAGGGAA ATCACTCCCA ATTAACGCGC GAACCCATAG AA
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FIG._11C